

FIG. 1A

10 30 50
 GAATTTCGGCACGAGCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGACATCA
 70 90 110
 ACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCCCCAA
 130 150 170
 CCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTAC
 M D D S T E R E Q S R L T
 190 210 230
 TTCTTGCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCCACG
 S C L K K R E E M K L K E C V S I L P R
 250 270 290
 GAAGGAAAGCCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCT
 K E S P S V R S S K D G K L L A A T L L
 310 330 350
 GCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCA
L A L L S C C L T V V S F Y O V A A L Q
 370 390 410
 AGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGC
 G D L A S L R A E L Q G H H A E K L P A
 430 450 470
 AGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACTGAA
 G A G A P K A G L E E A P A V T A G L K
 490 510 530
 AATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCG
 I F E P P A P G E G N S S Q N S R N K R
 550 570 590
 TGCCGTTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAGACAG
 A V Q G P E E T V T Q D C L Q L I A D S

FIG. 1B

610 630 650
 TGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAA
 E T P T I Q K G S Y T F V P W L L S F K
 670 690 710
 AAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTT
 R G S A L E E K E N K I L V K E T G Y F
 730 750 770
 TTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAATTCA
 F I Y G Q V L Y T D K T Y A M G H L I Q
 790 810 830
 GAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTTGTTCGATGTAT
 R K K V H V F G D E L S L V T L F R C I
 850 870 890
 TCAAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTCAGCTGGCATTTGCAAAACT
 Q N M P E T L P N N S C Y S A G I A K L
 910 930 950
 GGAAGAAGGAGATGAACTCCAATTGCAATACCAAGAGAAAATGCACAAATATCACTGGA
 E E G D E L Q L A I P R E N A Q I S L D
 970 990 1010
 TGGAGATGTCACATTTTTTGGTGCATTGAAACTGCTGTGACCTACTTACACCATGTCTGT
 G D V T F F G A L K L L
 1030 1050 1070
 AGCTATTTTCCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAA
 1090 1110 1130
 AAAAAAAAAAAAAAAAAAAAAAGTAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 1150 1170
 AAAAAAAAAAAAAAAAAAAAACTCGGAGGGGG

FIG. 2A

10 30 50
 GAATTCGGCACGAGCTCCAAAGGCCTAGACCTTCAAAGTGCTCCTCGTGGAATGGATGAG
 M D E
 70 90 110
 TCTGCAAAGACCCTGCCACCACCGTGCCTCTGTTTTTGCTCCGAGAAAGGAGAAGATATG
 S A K T L P P P C L C F C S E K G E D M
 130 150 170
 AAAGTGGGATATGATCCCATCACTCCGCAGAAGGAGGAGGGTGCCTGGTTTGGGATCTGC
 K V G Y D P I T P Q K E E G A W F G I C
 190 210 230
 AGGGATGGAAGGCTGCTGGCTGCTACCCTCCTGCTGGCCCTGTTGTCCAGCAGTTTCACA
 R D G R L L A A T L L L A L L S S S F T
 250 270 290
 GCGATGTCCTTGTACCAGTTGGCTGCCTTGCAAGCAGACCTGATGAACCTGCGCATGGAG
A M S L Y O L A A L Q A D L M N L R M E
 310 330 350
 CTGCAGAGCTACCGAGGTTTCAGCAACACCAGCCGCCGCGGTGCTCCAGAGTTGACCGCT
 L Q S Y R G S A T P A A A G A P E L T A
 370 390 410
 GGAGTCAAACCTCCTGACACCGGCAGCTCCTCGACCCCACTCCAGCCGCGGCCACAGG
 G V K L L T P A A P R P H N S S R G H R
 430 450 470
 AACAGACGCGCTTTCAGGGACCAGAGGAAACAGAACAAGATGTAGACCTCTCAGCTCCT
 N R R A F Q G P E E T E Q D V D L S A P
 490 510 530
 CCTGCACCATGCCTGCCTGGATGCCGCCATTCTCAACATGATGATAATGGAATGAACCTC
 P A P C L P G C R H S Q H D D N G M N L
 550 570 590
 AGAAACATCATTTCAAGACTGTCTGCAGCTGATTGCAGACAGCGACACGCCGACTATACGA
 R N I I Q D C L Q L I A D S D T P T I R

FIG. 2B

610 630 650
AAAGGAACTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGAGGAAATGCCTTGGAG
K G T Y T F V P W L L S F K R G N A L E
670 690 710
GAGAAAGAGAAACAAAATAGTGGTGAGGCAAACAGGCTATTTCTTCATCTACAGCCAGGTT
E K E N K I V V R Q T G Y F F I Y S Q V
730 750 770
CTATACACGGACCCCATCTTTGCTATGGGTCATGTCATCCAGAGGAAGAAAGTACACGTC
L Y T D P I F A M G H V I Q R K K V H V
790 810 830
TTTGGGGACGAGCTGAGCCTGGTGACCCTGTTCCGATGTATTCAGAATATGCCCAAACA
F G D E L S L V T L F R C I Q N M P K T
850 870 890
CTGCCCCAACAATTCCCTGCTACTCGGCTGGCATCGCGAGGCTGGAAGAAGGAGATGAGATT
L P N N S C Y S A G I A R L E E G D E I
910 930 950
CAGCTTGCAATTCCTCGGGAGAATGCACAGATTTACGCAACGGAGACGACACCTTCTTT
Q L A I P R E N A Q I S R N G D D T F F
970 990 1010
GGTGCCCTAAAACTGCTGTAACCTCACTTGCTGGAGTGCGTGATCCCCCTTCCCTCGTCTTC
G A L K L L
1030 1050 1070
TCTGTACCTCCGAGGGAGAAACAGACGACTGGAAAACTAAAAGATGGGGAAAGCCGTCA
1090 1110 1130
GCGAAAGTTTCTCGTGACCCGTTGAATCTGATCCAAACCAGGAAATATAACAGACAGCC
1150 1170 1190

FIG. 3A

	1				50
Hagp3	MDDSTER.EQ	SRLTSLCLKKR	EEMKLKECVS	ILPRKESPSV	RSSKDGKLLA
Magp3	MDESAKTLPP	PCLCFCSEKG	EDMKVGYPDPI	TPQKEEGAWF	GICRDGRLLA
cons	MD.S.....	..L..C..K.	E.MK.....	E.....DG.LLA
	51				100
Hagp3	<u>ATLLLLALLSC</u>	<u>CLTVVSFYOV</u>	<u>AALQGDLASL</u>	RAELQGHAE	KLPAGAGAPK
Magp3	<u>ATLLLLALLSS</u>	<u>SFTAMSLYOL</u>	<u>AALQADLMNL</u>	RMELQSYRGS	ATPAAAGAPE
cons	ATLLLLALLS.	..T..S.YQ.	AALQ.DL..L	R.ELQ.....	..PA.AGAP.
	101				150
Hagp3	AGLEEAPAVT	AGLKIFEPPA	PGEKNSSQNS	RNKRAVQGPE	ET.....
Magp3LT	AGVKLLTPAA	PRPHNSSRGH	RNRRAFQGPE	ETEQDVDLSA
consT	AG.K...P.A	P...NSS...	RN.RA.QGPE	ET.....
	151		B		200
Hagp3VTQDCLO	<u>LIADSETPTI</u>	QKGSYTFVPW
Magp3	PPAPCLPGCR	HSQHDDNGMN	LRNIIQDCLO	<u>LIADSDTPTI</u>	RKGTYTFVPW
consQDCLO	LIADS.TPTI	.KG.YTFVPW

FIG. 3B

	B'	C'	C	D	E	250
Hagp3	<u>LLSEFKRG</u> SAL	<u>EEKENKIL</u> VK	ETGYFFFIYGO	<u>VL</u> YTDKTYAM	<u>GH</u> LIQRKKVH	
Magp3	<u>LLSEFKRG</u> NAL	<u>EEKENKI</u> VVR	QTGYFFFIYSO	<u>VL</u> YTDPIFAM	<u>GH</u> VIQRKKVH	
cons	LLSEFKRG.AL	EEKENKI.V.	.TGYYFFIY.Q	VLYTD...AM	GH.IQRKKVH	
	F	G	H			300
Hagp3	<u>VFGDEL</u> SLVT	<u>LFRCIQ</u> NMPE	<u>TL</u> PNNSCYSA	<u>GIAK</u> LEEGDE	<u>LO</u> LAIPRENA	
Magp3	<u>VFGDEL</u> SLVT	<u>LFRCIQ</u> NMPK	<u>TL</u> PNNSCYSA	<u>GIA</u> RLEEGDE	<u>IOL</u> AIPRENA	
cons	VFGDELSLVT	LFRCIQNMP.	<u>TL</u> PNNSCYSA	GIA.LEEGDE	.QLAIPRENA	
	I					317
Hagp3	QISLDGDVTF	<u>FGAL</u> KLL				
Magp3	QISRNGDDTF	<u>FGAL</u> KLL				
cons	QIS..GD.TF	FGALKLL				

FIG. 4A

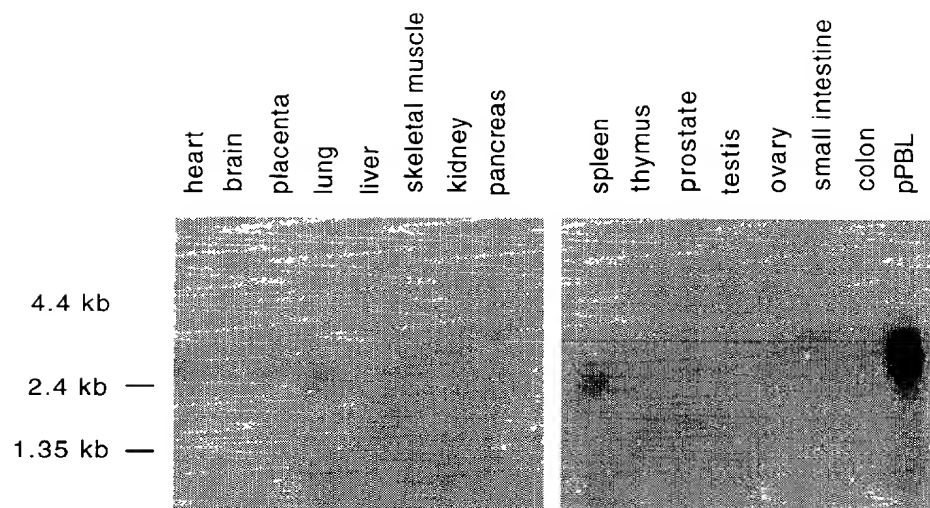


FIG. 4B

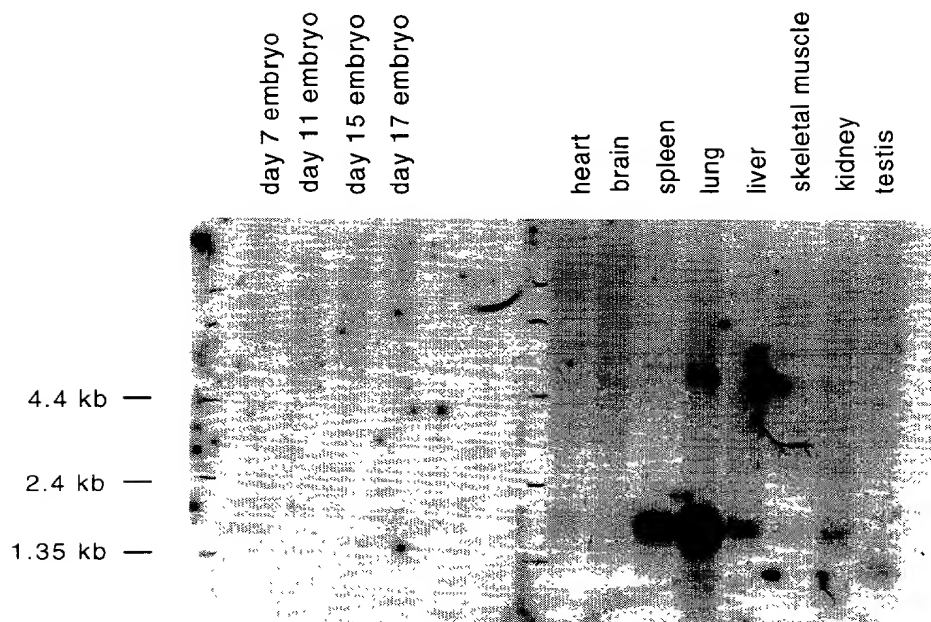


FIG. 5A

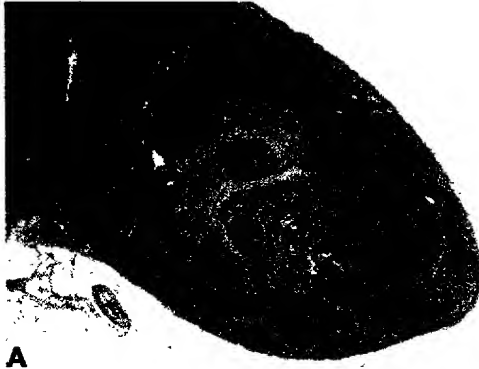


FIG. 5B

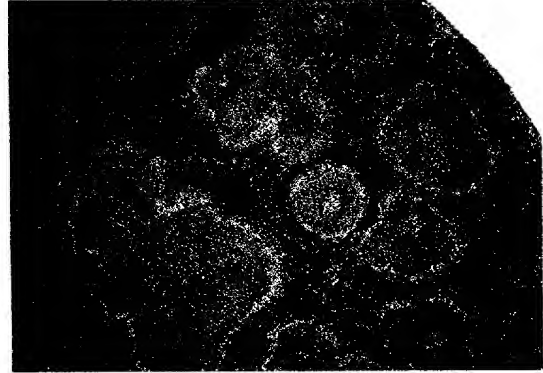


FIG. 5C

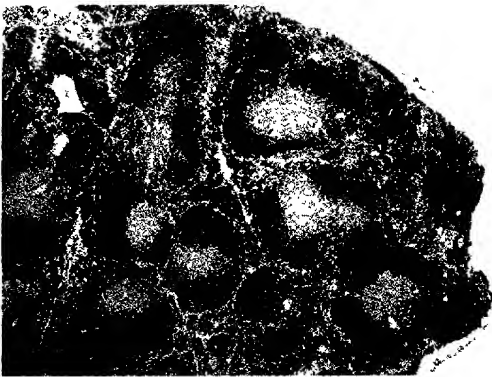


FIG. 5D

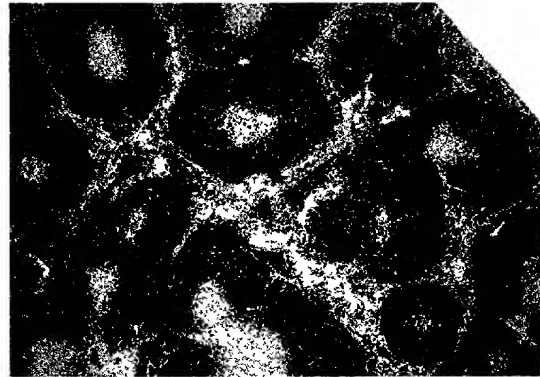


FIG. 5E

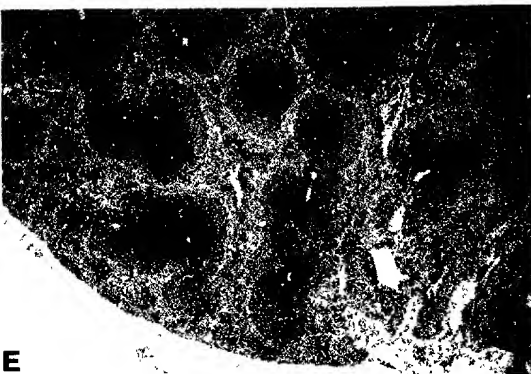


FIG. 5F

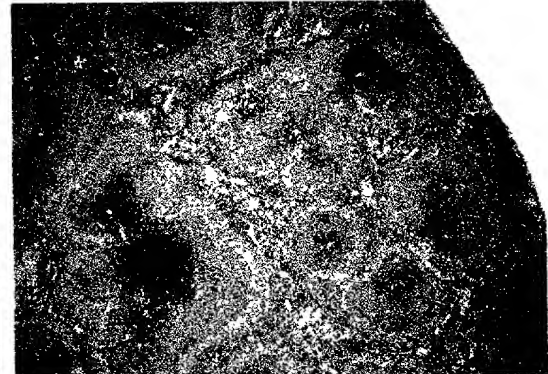


FIG. 6A

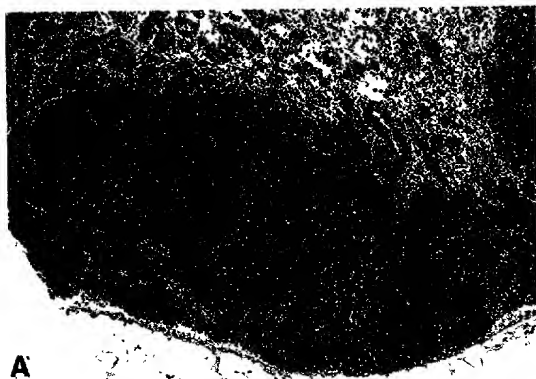


FIG. 6B



FIG. 6C



FIG. 6D

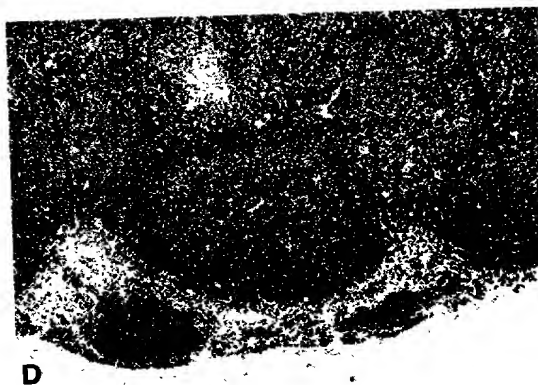


FIG. 6E



FIG. 6F

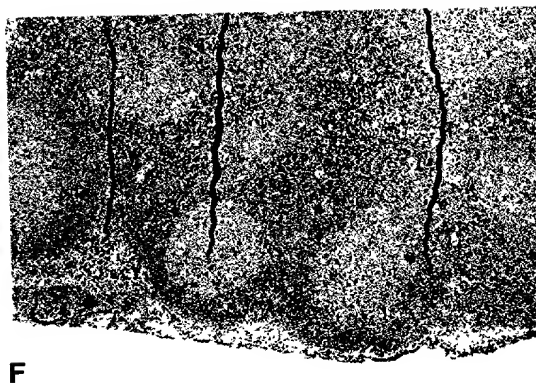
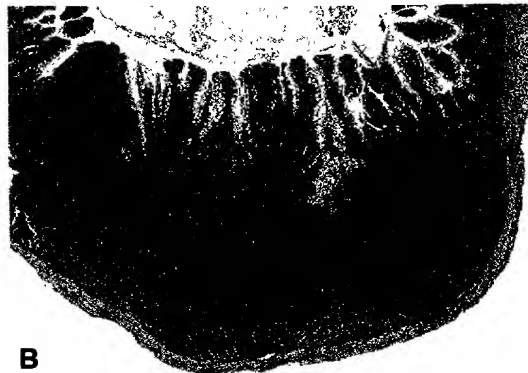


FIG. 7A



A

FIG. 7B



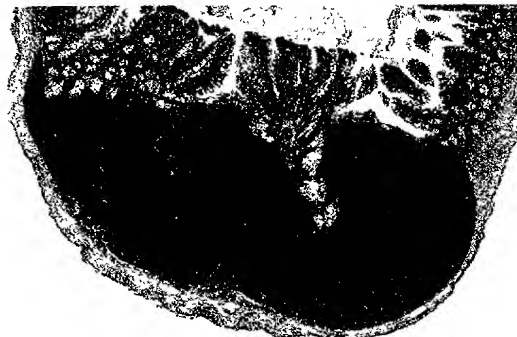
B

FIG. 7C



C

FIG. 7D



D

FIG. 7E



E

FIG. 7F



F

FIG. 8A

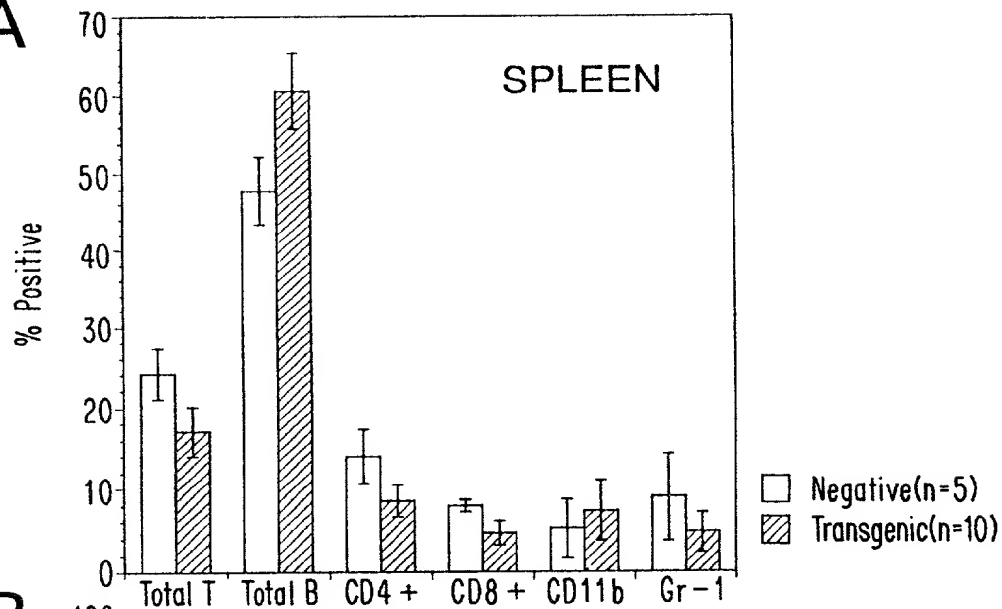


FIG. 8B

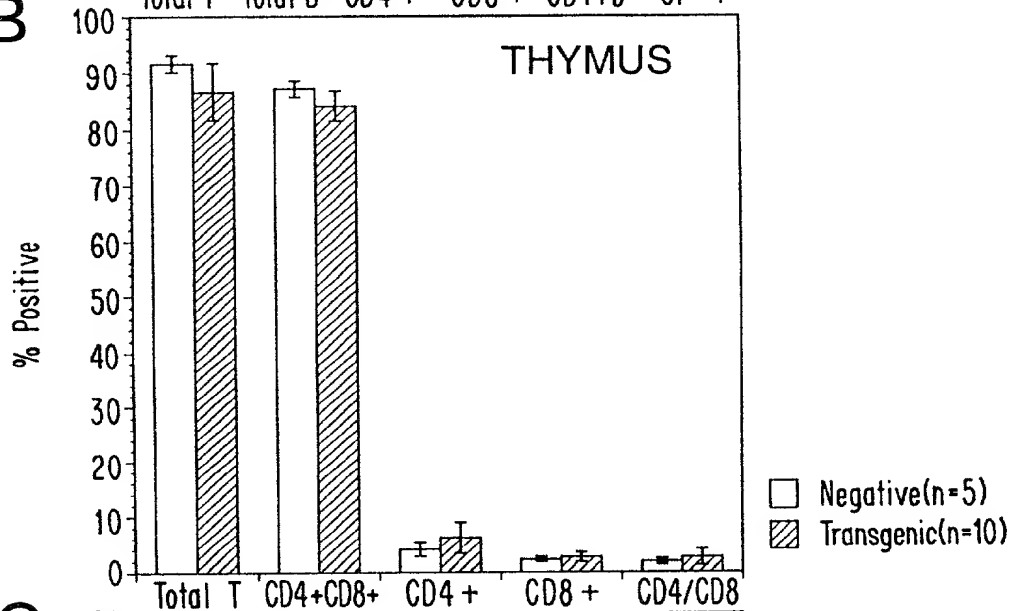


FIG. 8C

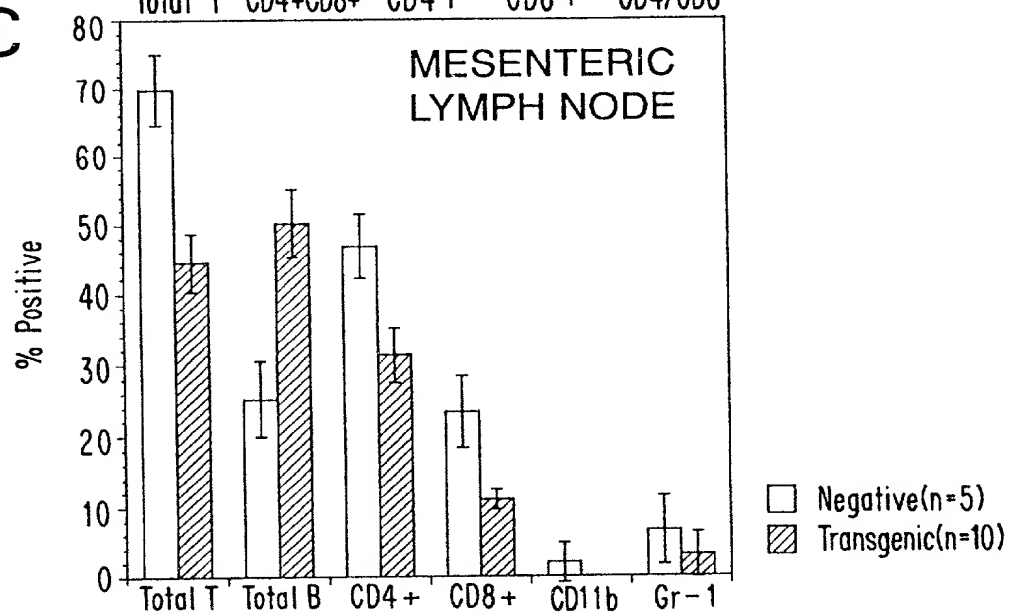


FIG. 9A

	B	B/B' loop	B'	C'	C	D	D/E loop	E	
	---+PAAHLT--P	---	---	---	---	---	---	---	Consensus
	---	---	L-W	A-LS-GV-L-N	---	LW	GLYFIYSQV-F+GQ-CP	---	Human FasL
139-	EKKELRKVAHLTGKSN	---	SRS-MPLEWEDTYGI	VLLS-GVKYKK	---	GGLV	NETGLYFVYSKVYFRGQSCN	---	Mouse FasL
137-	EKKEPRVAHLTGKSN	---	SRS-IPLEWEDTYGT	ALIS-GVKYKK	---	GGLV	NETGLYFVYSKVYFRGQSCN	---	Rat FasL
136-	ETKKPRVAHLTGKSN	---	SRS-IPLEWEDTYGT	ALIS-GVKYKK	---	GGLV	INEAGLYFVYSKVYFRGQSCN	---	Human CD40L
116-	GDQNPQIAAHVISEASS	---	KTT-SVLQWAEKGY	TMSNNLVTLENG	---	KQLTVKRQGLYIYAQVTFCSNREA	---	Mouse CD40L	
115-	GDQNPQIAAHVISEANS	---	NAA-SVLQWAKKGY	TMSNNLVTLENG	---	KQLTVKRQGLYIYAQVTFCSNREP	---	Human AGP3	
142-	---	---	---	---	---	KIL-VKETGYFFIYSQVLYT-DKT	---	Mouse AGP3	
163-	---	---	---	---	---	KIL-VKETGYFFIYSQVLYT-DPI	---	Mouse OPGL	
157-	---	---	---	---	---	KIL-VKETGYFFIYSQVLYT-DPI	---	Human OPGL	
158-	---	---	---	---	---	KIL-VKETGYFFIYSQVLYT-DPI	---	Human TRAIL	
116-	ERGPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGH-SFLSN-LHLRNG-E-LVIEHEKGFYIYSQTYFRFQEE	---	---	---	---	K-LRVNODGFYLYANICFRHHETS	---	Mouse TRAIL	
120-	GRPQKVAHITGITRRSNSALIPISKDGKTLGQKIESWESSRKGH-SFLNH-VLFRNG-E-LVIEQEGLYIYSQTYFRFQEAEDASKMVSKD	---	---	---	---	K-LRVNODGFYLYANICFRHHETS	---	Human CD30L	
92-	RAPFKKSWAYLQVAKH	---	---	---	---	K-LRVNODGFYLYANICFRHHETS	---	Mouse CD30L	
97-	STPSKKSWAYLQVSKH	---	---	---	---	K-LRVNODGFYLYANICFRHHETS	---	Human Lytβ	
82-	DLSPGLPAAHLIGAP	---	---	---	---	K-LRVNODGFYLYANICFRHHETS	---	Mouse Lytβ	
148-	DLNPGLPAAHLIGAW	---	---	---	---	K-LRVNODGFYLYANICFRHHETS	---	Human TNFβ	
57-	AHSTLKPAHLIGDP	---	---	---	---	K-LRVNODGFYLYANICFRHHETS	---	Mouse TNFβ	
54-	THGILKPAHLVGYP	---	---	---	---	K-LRVNODGFYLYANICFRHHETS	---	Human TNFα	
82-	RTPSDKPVAHVVANP	---	---	---	---	K-LRVNODGFYLYANICFRHHETS	---	Mouse TNFα	
85-	QNSDDKPVAVHVANH	---	---	---	---	K-LRVNODGFYLYANICFRHHETS	---		

FIG. 9B

E	E/F loop	F	F/G loop	G	H	H/I loop	I
208-	-H-V---V-----YP-----LLS---T---C-----W-S-YLGGVF-L--GD-LYVNV---S---F-----TFFGLFKL						-281 Human FasL
206-	SHKVYMRNS-----KYPQDLVMMEGKMMSYC-----TTGQMWARSSYLGAVENTSADHLYVNVSELSLVNFEESQ-TFFGLYKL						-279 Mouse FasL
205-	NHKVYMRNS-----KYPEDLVIMEEKRLNYC-----TTGQIWAHSSYLGAVENTSADHLYVNIQSLSLINFEESK-TFFGLYKL						-278 Rat FasL
190-	SHKVYMRNF-----KYPGDLVIMEEKKLNYC-----TTGQIWAHSSYLGAVENTVADHLYVNIQSLSLINFEESK-TFFGLYKL						-261 Human CD40L
189-	IASLCLKS-----PGRFERILLRAANTHSSAKPC-----GQOSIHLLGGVFELQPGASVFVNVTDPQSQVSHGTGF-TSFGLLKL						-260 Mouse CD40L
212-	IVGLWLKP-----SIGSERILLKAANTHSSQLC-----EQQSVHLGGVFELQAGASVFVNVTASQVIHRVGF-SSFGLLKL						-285 Human AGP3
212-	IQRKKVHV-----FGDELSLVTLFRCIQNMPETL-----P--NNSCY SAGIARLEEGDEIQLAIPRENAQISLDGDTVTFGALKLL						-309 Mouse AGP3
236-	IQRKKVHV-----FGDELSLVTLFRCIQNMPKTL-----P--NNSCY SAGIARLEEGDEIQLAIPRENAQISLDGDTVTFGALKLL						-316 Mouse OPGL
234-	YLQLMVYVTKTSI--KIPSSHNLMKGGSTKNWSGN-----SE--FHFYSINVGFFKL RAGEEISIQVNSPSLLDPDQDA-TYFGAFKVQDID						-317 Human OPGL
235-	YLQLMVYVTKTSI--KIPSSHNLMKGGSTKNWSGN-----SE--FHFYSINVGFFKL RAGEEISIEVSNPSLLDPDQDA-TYFGAFKVRDID						-281 Human TRAIL
201-	K-NDKQMVQYIYKTSYDPDPIVLMKSARNSCWSKD-----AE--YGLYSIYQG GIFFELKENDRIFVSVTNEHLIDMDHEA-SFFGAFLV						-291 Mouse TRAIL
210-	KVRTKQLVQYIYKTSYDPDPIVLMKSARNSCWSKD-----AE--YGLYSIYQG GIFFELKENDRIFVSVTNEHLIDMDHEA-SFFGAFLIN						-234 Human CD30L
159-	KLELLIN-----KHKKQALVTVCESGMQTK--HVYQNL SQFLLDYLVQNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD						-239 Mouse CD30L
164-	TLQLLIN-----SKIKKQTLVTVCESGVQSK--NIYQNL SQFLLDYLVQNTTISVNVDTFQYIDTSTFPLENVLSVFLYSSSD						-244 Human LyT β
158-	TLRSSLYRAGGA--YGPGTPEL LLEGAETVTPVLDPARRQGYGPIWYTSVGFGLVQLRRGERVYVNI SHPDMVDFARGK-TFFGAVMVG						-306 Mouse LyT β
223-	TLRSALYRAGGA--YGRGSPELL LLEGAETVTPVVDPI---GYGSLWYTSVGFGLAQLRSGERVYVNI SHPDMVDRARGK-TFFGAVMVG						-205 Human TNF β
132-	AHEVQLFSS-----QYPFHVPLLSQKSMVYP-----GLQEPWLHSMYHGA AFQLTQGDQLSTHTDGI PHLVLS PST-VFFGAFAL						-202 Mouse TNF β
129-	AHEVQLFSS-----QYPFHVPLLSQKSMVYP-----GLQEPWLHSMYHGA AFQLTQGDQLSTHTDGI SHLHFS PSS-VFFGAFAL						-233 Human TNF α
153-	THTISRIV-----SYQTKVNLLSAIKSPQRETPEG--AEAKPWYEP IYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGI AL						-235 Mouse TNF α
155-	THTVSRFAI-----SYQEKVNLLSAVKSPKDTPEG--AELKPWYEP IYLGGVFQLEKGDQLSAEVLNPKYLDFAESGQVYFGVIAL						

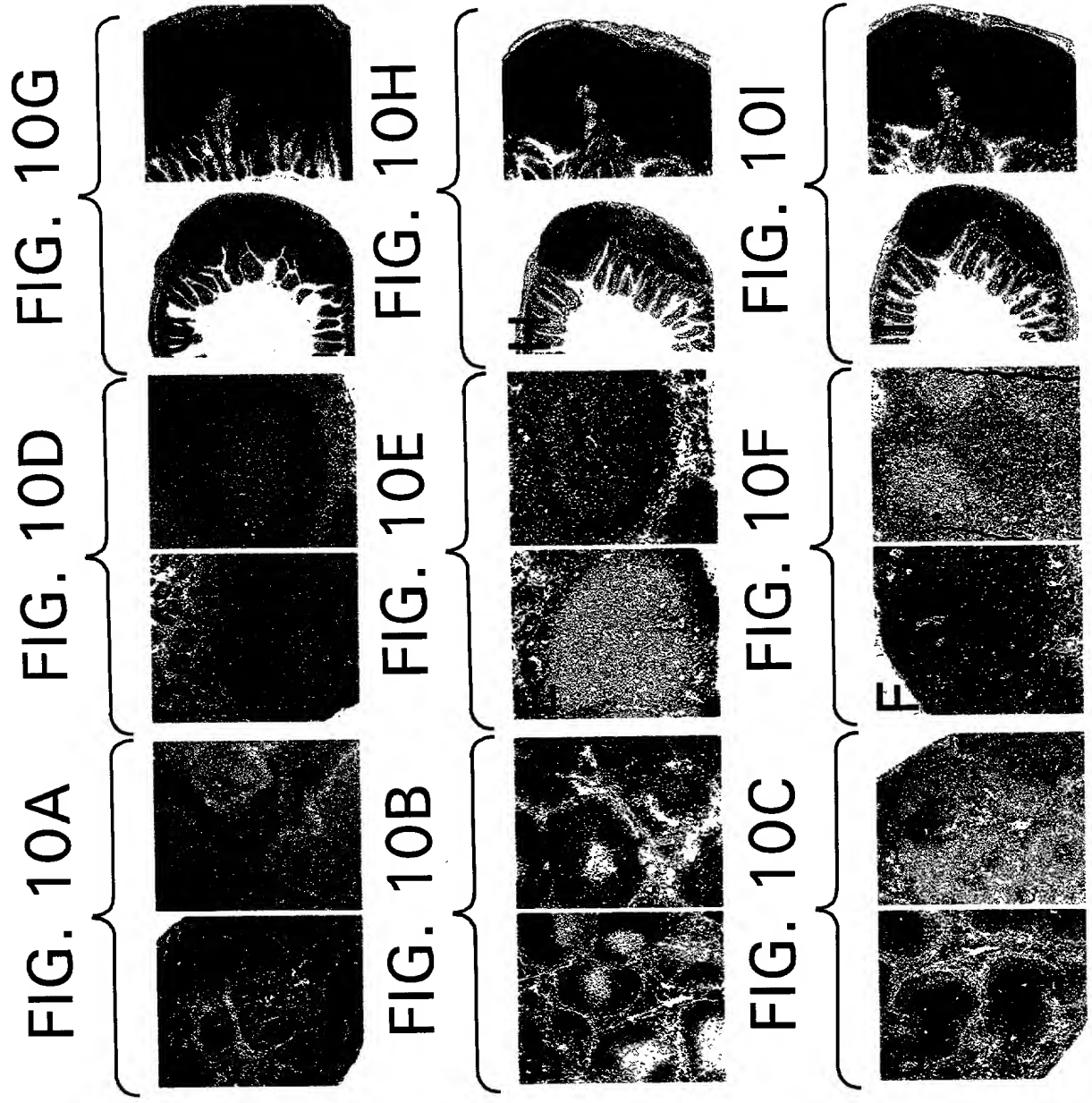


FIG. 11A

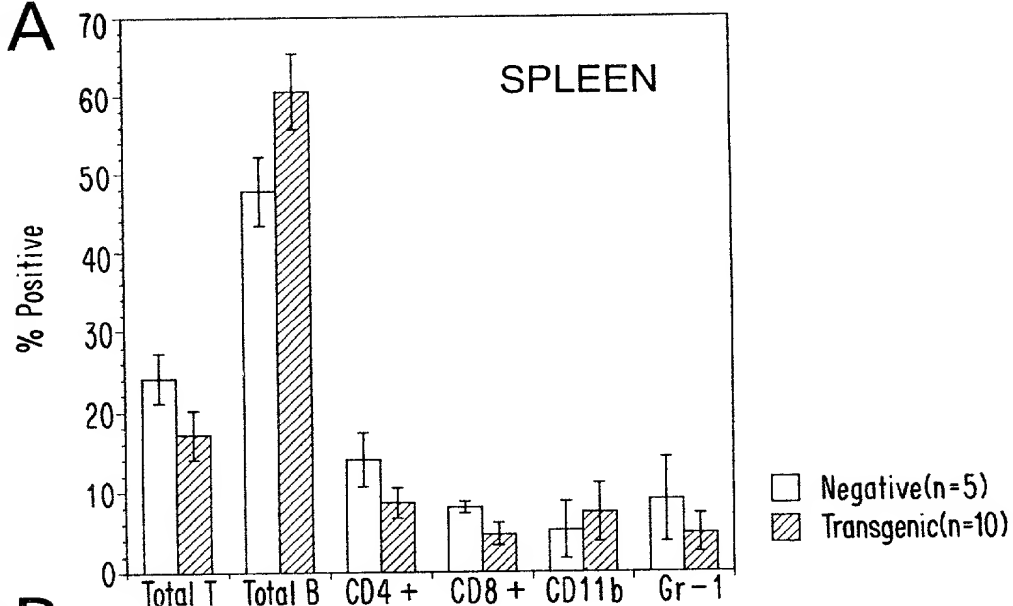


FIG. 11B

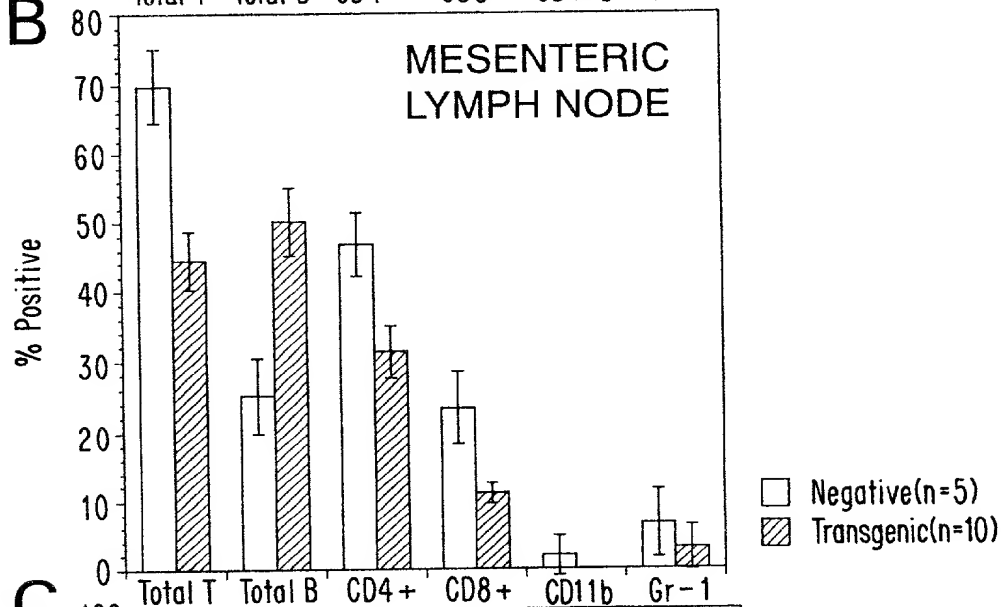


FIG. 11C

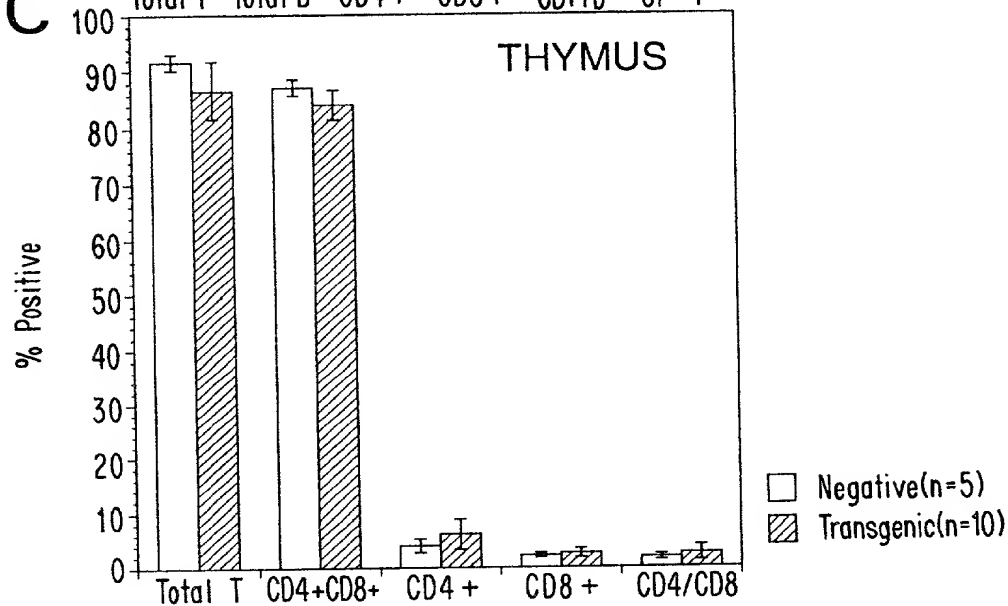


FIG. 12A

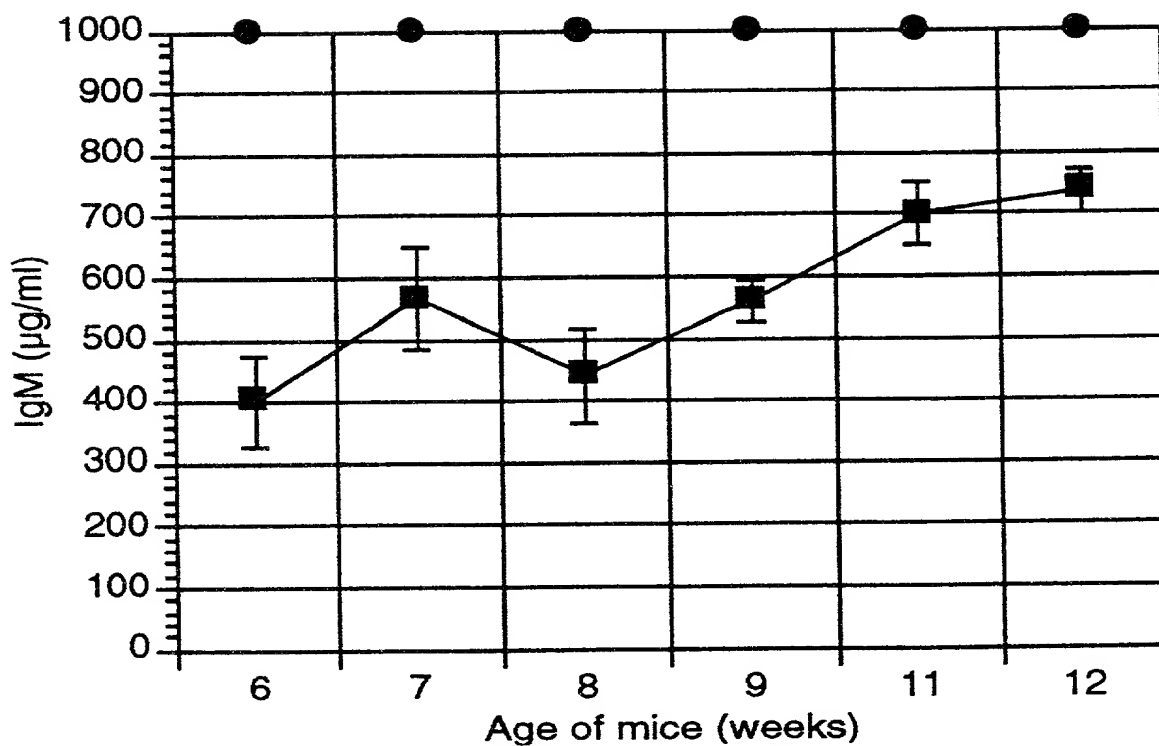


FIG. 12B

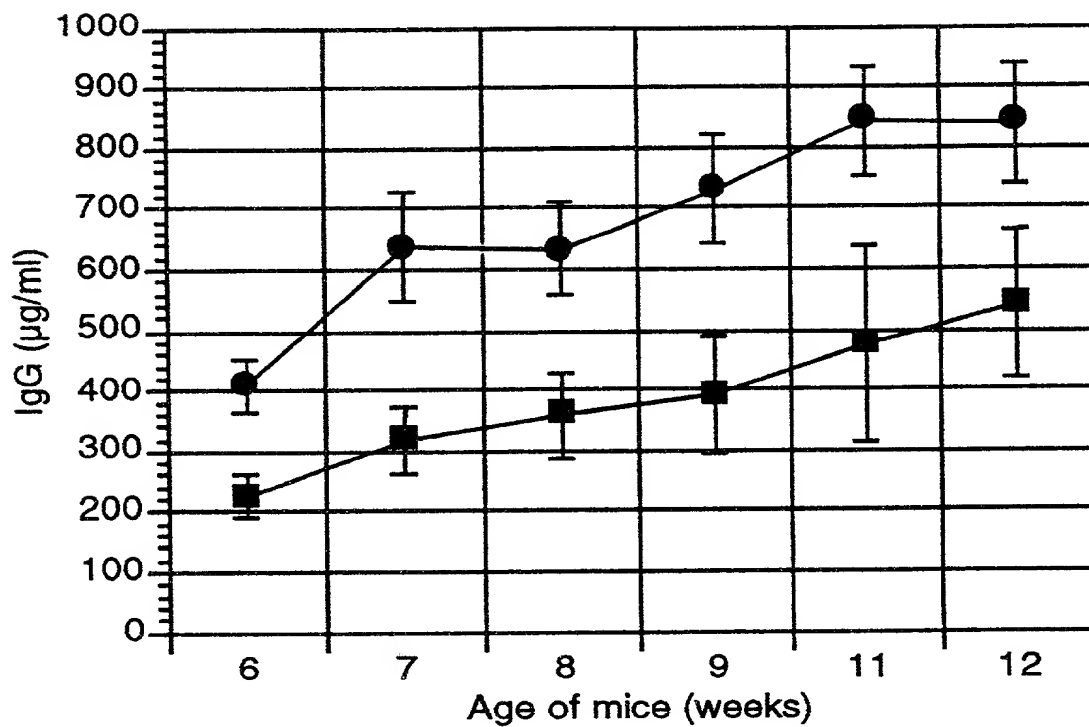


FIG. 12C

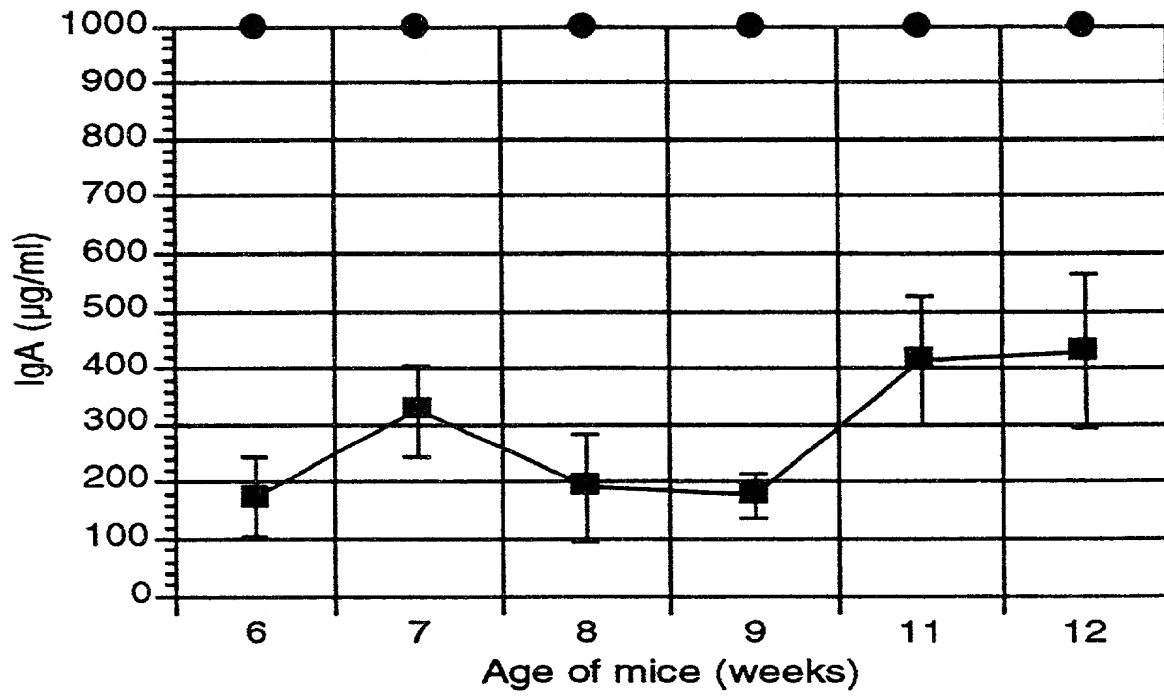


FIG. 12D

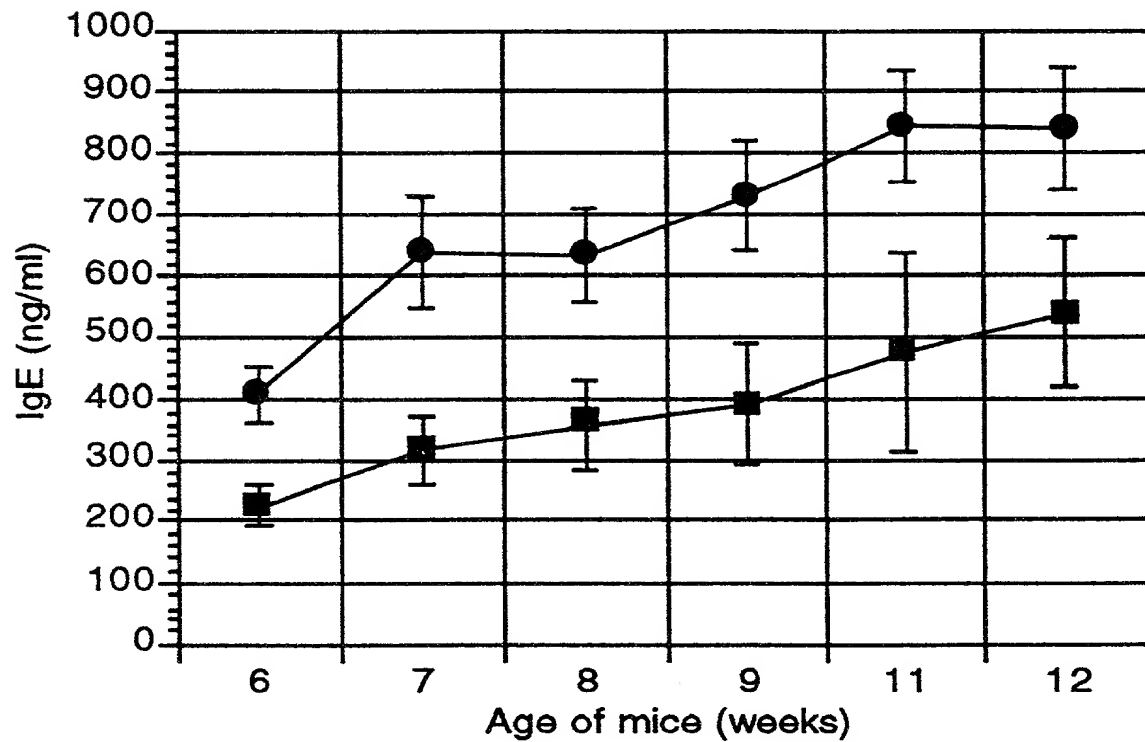


FIG. 13A

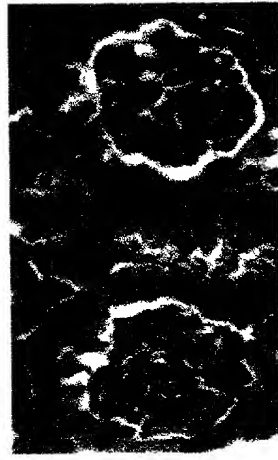


FIG. 13D



FIG. 13G

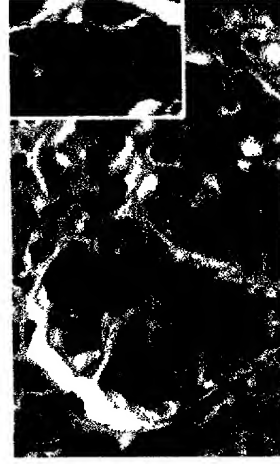


FIG. 13B



FIG. 13E

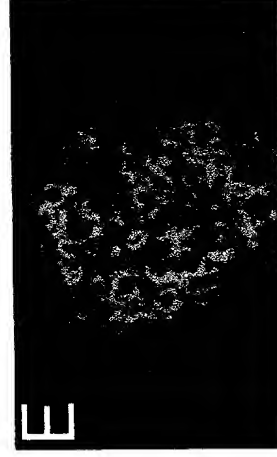


FIG. 13H

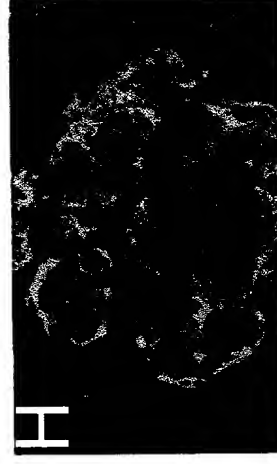


FIG. 13C



FIG. 13F



FIG. 13I

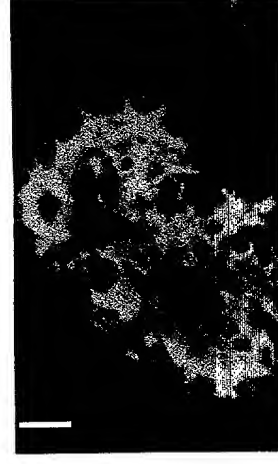


FIG. 14A

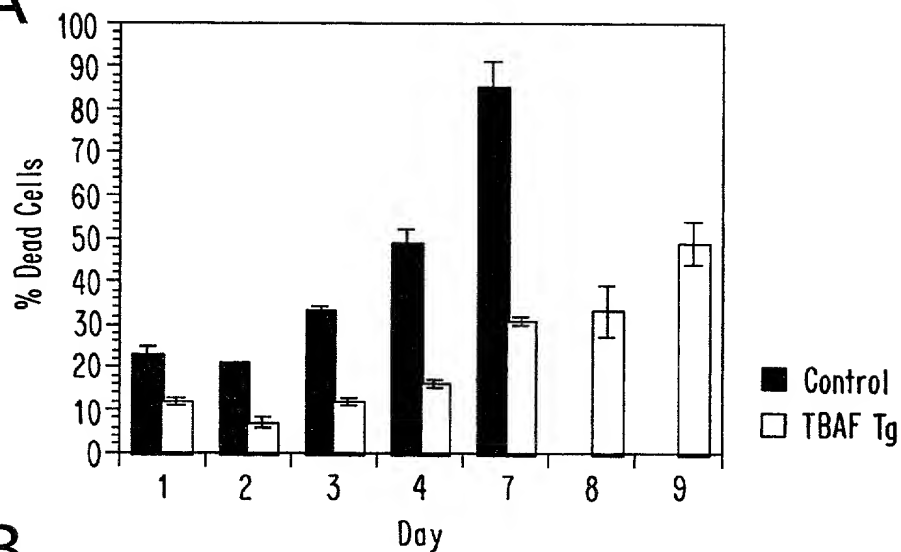


FIG. 14B

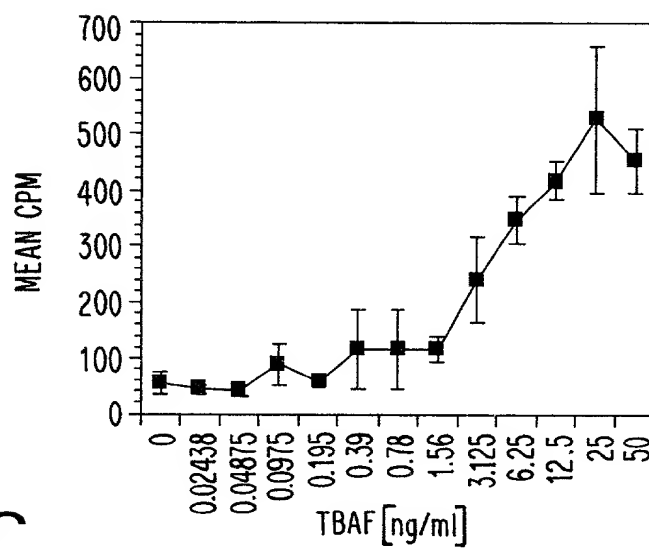


FIG. 14C

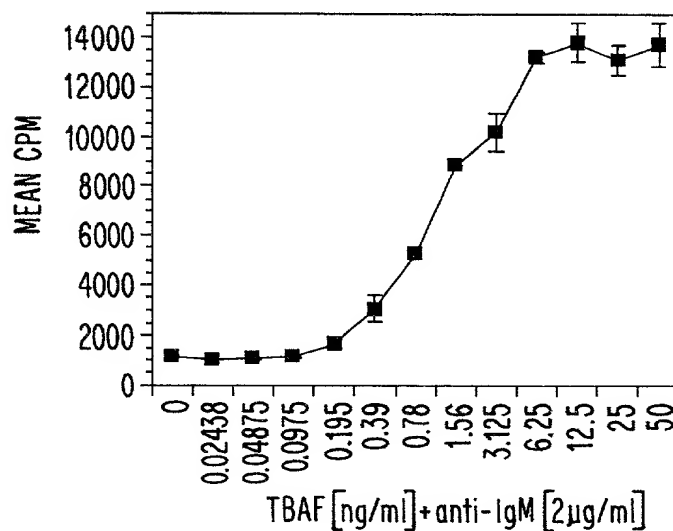


FIG. 15

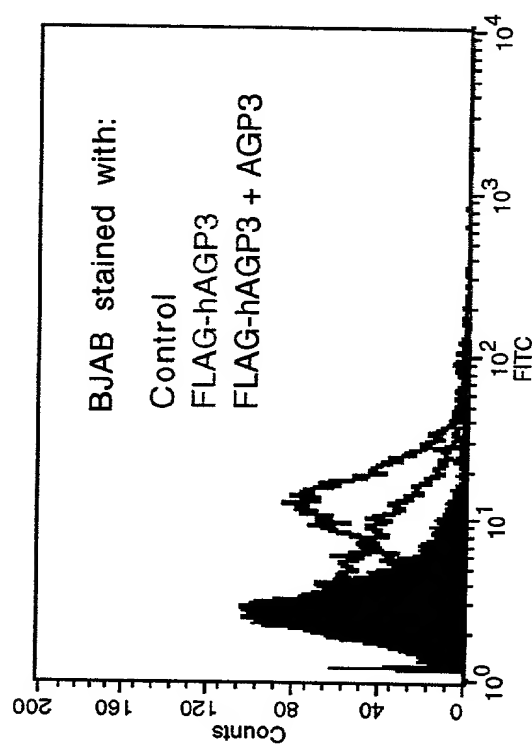
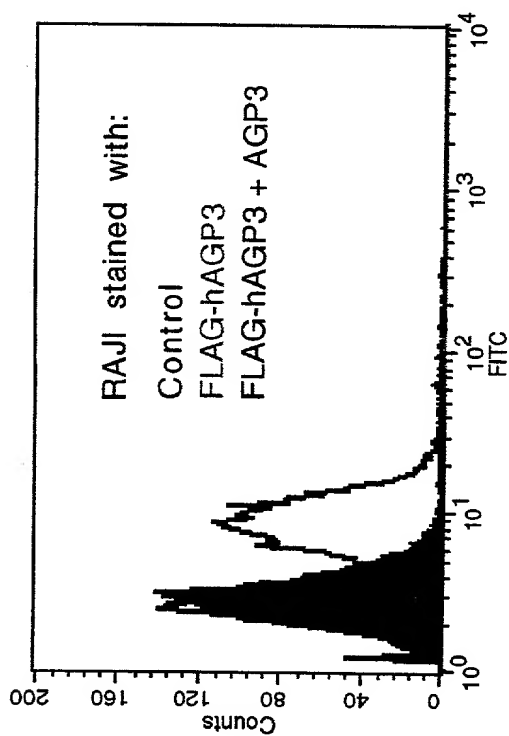
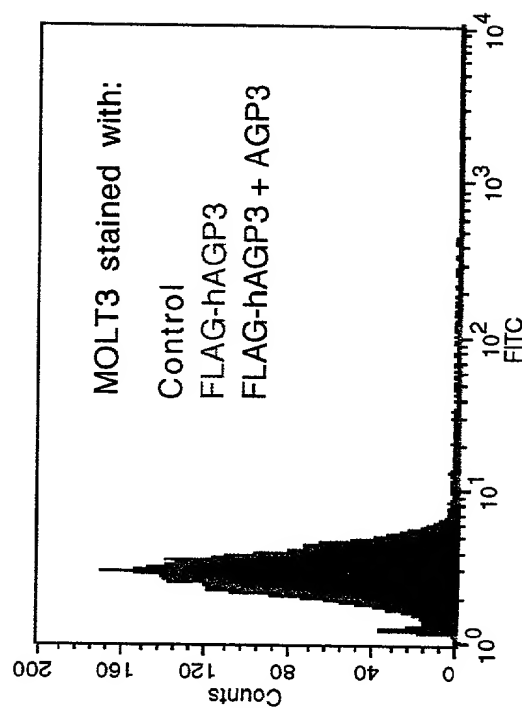
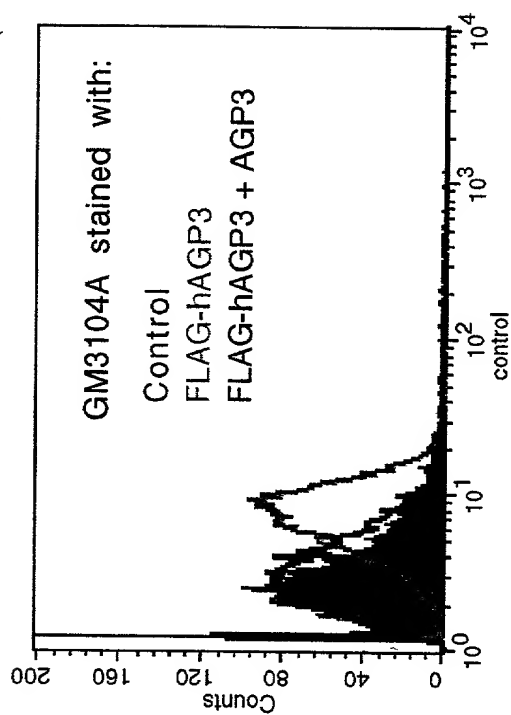


FIG. 16

Alignment of AGP3-binding pools 13B4 and 13H11
N-terminal sequence

```

1  GTCGACCCACGCGTCCG.....ATCCTGAGTAATGAGTGGCCTGGGCC 43
   |||||||||||||||||
1  GTCGACCCACGCGTCCGAATAAGCATCCTGAGTAATGAGTGGCCTGGGCC 50
   |||||||||||||||||

44  GGAGCAGGCGAGGTGGCCGGAGCCGTGTGGACCAGGAGGAGCGCTTTCCA 93
   |||||||||||||||||
51  GGAGCAGGCGAGGTGGCCGGAGCCGTGTGGACCAGGAGGAGCGCTTTCCA 100
   |||||||||||||||||

94  CAGGGCCTGTGGACAGGGGTGGCTATGAGATCCTGCCCCGAAGAGCAGTA 143
   |||||||||||||||||
101 CAGGGCCTGTGGACAGGGGTGGCTATGAGATCCTGCCCCGAAGAGCAGTA 150
   |||||||||||||||||

144 CTGGGATCCTCTGCTGGGTACCTGCATGTCCTGCAAAACCATTGCAACC 193
   |||||||||||||||||
151 CTGGGATCCTCTGCTGGGTACCTGCATGTCCTGCAAAACCATTGCAACC 200
   |||||||||||||||||

194 ATCAGAGCCAGCGCACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGCCGC 243
   |||||||||||||||||
201 ATCAGAGCCAGCGCACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGCCGC 250
   |||||||||||||||||

244 AAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTG 293
   |||||||||||||||||
251 AAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTG 300
   |||||||||||||||||

294 TGCCTCCATCTGTGGACAGCACCTAAGCAATGTGCATACTTCTGTGAGA 343
   |||||||||||||||||
301 TGCCTCCATCTGTGGACAGCACCTAAGCAATGTGCATACTTCTGTGAGA 350
   |||||||||||||||||

344 ACAAGCTCAGGAGCCCAGTGAACCTTCCACCAGAGCTCAGGAGACAGCGG 393
   |||||||||||||||||
351 ACAAGCTCAGGAGCCCAGTGAACCTTCCACCAGAGCTCAGGAGACAGCGG 400
   |||||||||||||||||

```

FIG. 17

Human AGP3 receptor sequence

GTCTGACCCACGCGTCCGATCCTGAGTAATGAGTGGCCTGGGCCGGAGCAGGCGAGGTGGC
M S G L G R S R R G G
CGGAGCCGTGTGGACCAGGAGGAGCGCTTTCCACAGGGCCTGTGGACAGGGGTGGCTATG
R S R V D Q E E R F P Q G L W T G V A M
AGATCCTGCCCCGAAGAGCAGTACTGGGATCCTCTGCTGGGTACCTGCATGTCCTGCAAA
R S C P E E Q Y W D P L L G T C M S C K
ACCATTGCAACCATCAGAGCCAGCGCACCTGTGCAGCCTTCTGCAGGTCACTCAGCTGC
T I C N H Q S Q R T C A A F C R S L S C
CGCAAGGAGCAAGGCAAGTTCTATGACCATCTCCTGAGGGACTGCATCAGCTGTGCCTCC
R K E Q G K F Y D H L L R D C I S C A S
ATCTGTGGACAGCACCTAAGCAATGTGCATACTTCTGTGAGAACAGCTCAGGAGCCCA
I C G Q H P K Q C A Y F C E N K L R S P
GTGAACCTTCCACCAGAGCTCAGGAGACAGCGGAGTGAGAAAGTTGAAAACAATTGAGAC
V N L P P E L R R Q R S G E V E N N S D
AACTCGGGAAGGTACCAAGGACTGGAGCACAGAGGCTCAGAAGCAAGTCCAGCTCTCCCG
N S G R Y Q G L E H R G S E A S P A L P
GGGCTGAAGCTGAGTGCAGATCAGGTGGCCCTGGTCTACAGCACGCTGGGGCTCTGCCTG
G L K L S A D Q V A L V Y S T L G L C L
TGTGCCGTCTCTGCTGCTTCTGGTGGCGGTGGCCTGCTTCTCAAGATGAGGGGGGAT
C A V L C C F L V A V A C F L K M R G D
CCCTGCTCCTGCCAGCCCCGCTCAAGGCCCGCTCAAAGTCCGGCCAAGTCTTCCAGGAT
P C S C Q P R S R P R Q S P A K S S Q D
CACGCGATGGAAGCCGGCAGCCCTGTGAGCACATCCCCGAGCCAGTGGAGACCTGCAGC
H A M E A G S P V S T S P E P V E T C S
TTCTGCTTCCCTGAGTGCAGGGCGCCACGCAGGAGAGCGCAGTCACGCCTGGGACCCCC
F C F P E C R A P T Q E S A V T P G T P
GACCCCACTTGTGCTGGAAGGTGGGGGTGCCACACCAGGACCACAGTCCTGCAGCCTTGC
D P T C A G R W G C H T R T T V L Q P C
CCACACATCCCAGACAGCGGCCCTTGGCATTGTGTGTGTGCCTGCCAGGAGGGGGGCCCA
P H I P D S G L G I V C V P A Q E G G P
GGTGCATAAATGGGGGTCAGGGAGGGAAGGAGGAGGAGAGATGGAGAGGAGGGGAG
G A
AGAGAAAGAGAGGTGGGGAGAGGGGAGAGAGATATGAGGAGAGAGAGACAGAGGAGGCAG
AGAGGGAGAGAAACAGAGGAGACAGAGAGGGAGAGAGACAGAGGGAGAGAGAGACAGA
GAGGAAGAGAGGCAGAGAGGGAAAGAGGCAGAGAAGGAAAGAGACAGGCAGAGAAGGAGA
GAGGCAGAGAGGGAGAGAGGCAGAGAGGGAGAGAGGCAGAGAGACAGAGAGGGAGAGAGG
GACAGAGAGAGATAGAGCAGGAGGTGGGGCACTCTGAGTCCCAGTCCCAGTGCAGCTG
TAGGTCGTCATCACCTAACCAACAGTGCATAAAGTCCTCGTGCCTGCTGCTCACAGCCC
CCGAGAGCCCCCTCCTCCTGG

FIG. 18

AGP3 receptor protein structure

MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMR

SCPEEQYWDPLLGTCSCKTICNHQSQRRTCAAFCSRSL I

SCRKEQGKFYDHLLRDCISCASICGQHPKQCAYFCENK II

LRSPVNLPPPELRRQRSGEVENNSDNGRYQGLEHRGSE stalk
ASPALPGLKLSADQVAVYS

TLGLCLCAVLCCFLVAVACFL TM

KMRGDPCSCQPRSRPRQSPAKSSQDHAMEAGSPVSTSP IC
EPVETCSFCFPECRAPTQESAVTPGTPDTCAGRWCHT
RTTVLQPCPHIPDSGLGIVCVPAQEGGPGA

FIG. 19

Alignment of AGP3 receptor and TNFR1 extracellular domain

10	20	30	40	50	60	
LGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTTCMSCKTICNHQS-QR						AGP3R
: : : : : : :						
VLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIHPQNNNSIC--C-TKCHKGTLYN						TNFR1
20	30	40	50	60	70	
70	80	90	100	110		
TCAAFCRSLSCRK-EQGKF-YDHLLRDCISCASICGQHPKQCA YFCENKL RSPVNL PPE						AGP3R
: : : : : : : : : :						
DCPGPGQD TDCRECESGSFTASENHLRHCLSC-SKCRKEMGQVEISSCTVDRD TVCGCRK						TNFR1
80	90	100	110	120		

FIG. 20

Human AGP3 receptor mRNA tissue distribution

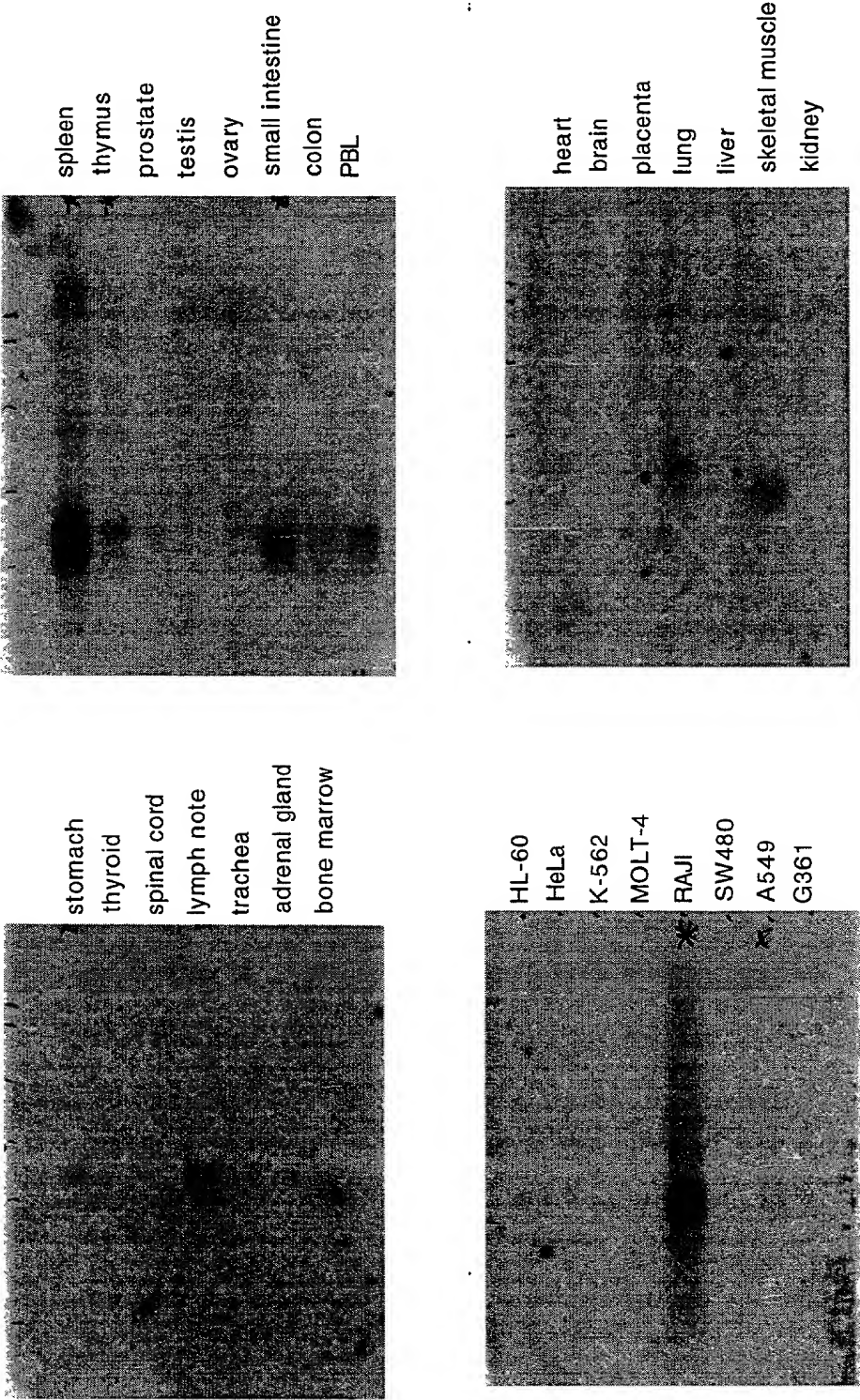


FIG 21

